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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=5; day=21; hr=12; min=12; sec=30; ms=648;]

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Application No: 10598736 Version No: 1.1

Input Set:

Output Set:

Started: 2008-05-21 12:10:04.804
Finished: 2008-05-21 12:10:05.727
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 923 ms
Total Warnings: 9
Total Errors: 0
No. of SeqIDs Defined: 9
Actual SeqID Count: 9

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W 402	Undefined organism found in <213> in SEQ ID (9)

SEQUENCE LISTING

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SANOFI-AVENTIS

<120> USE OF ANTAGONISTS TO THE CB1 RECEPTOR FOR THE MANUFACTURE
OF A COMPOSITION USEFUL FOR THE TREATMENT OF HEPATIC DISEASES

<130> CB1

<140> 10598736

<141> 2008-05-07

<150> EP04290633

<151> 2004-03-09

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 472

<212> PRT

<213> Human

<400> 1

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			20					25					30		

Ile	Lys	Gly	Asp	Met	Ala	Ser	Lys	Leu	Gly	Tyr	Phe	Pro	Gln	Lys	Phe
		35						40					45		

Pro	Leu	Thr	Ser	Phe	Arg	Gly	Ser	Pro	Phe	Gln	Glu	Lys	Met	Thr	Ala
	50						55					60			

Gly Asp Asn Pro Gln Leu Val Pro Ala Asp Gln Val Asn Ile Thr Glu
65 70 75 80

Phe Tyr Asn Lys Ser Leu Ser Ser Phe Lys Glu Asn Glu Glu Asn Ile
85 90 95

Gln Cys Gly Glu Asn Phe Met Asp Ile Glu Cys Phe Met Val Leu Asn
100 105 110

Pro Ser Gln Gln Leu Ala Ile Ala Val Leu Ser Leu Thr Leu Gly Thr
115 120 125

Phe Thr Val Leu Glu Asn Leu Leu Val Leu Cys Val Ile Leu His Ser
130 135 140

Arg Ser Leu Arg Cys Arg Pro Ser Tyr His Phe Ile Gly Ser Leu Ala
145 150 155 160

Val Ala Asp Leu Leu Gly Ser Val Ile Phe Val Tyr Ser Phe Ile Asp
165 170 175

Phe His Val Phe His Arg Lys Asp Ser Arg Asn Val Phe Leu Phe Lys
180 185 190

Leu Gly Gly Val Thr Ala Ser Phe Thr Ala Ser Val Gly Ser Leu Phe
195 200 205

Leu Thr Ala Ile Asp Arg Tyr Ile Ser Ile His Arg Pro Leu Ala Tyr
210 215 220

Lys Arg Ile Val Thr Arg Pro Lys Ala Val Val Ala Phe Cys Leu Met
225 230 235 240

Trp Thr Ile Ala Ile Val Ile Ala Val Leu Pro Leu Leu Gly Trp Asn
245 250 255

Cys Glu Lys Leu Gln Ser Val Cys Ser Asp Ile Phe Pro His Ile Asp
260 265 270

Glu Thr Tyr Leu Met Phe Trp Ile Gly Val Thr Ser Val Leu Leu Leu
275 280 285

Phe Ile Val Tyr Ala Tyr Met Tyr Ile Leu Trp Lys Ala His Ser His

290

295

300

Ala Val Arg Met Ile Gln Arg Gly Thr Gln Lys Ser Ile Ile Ile His
305 310 315 320

Thr Ser Glu Asp Gly Lys Val Gln Val Thr Arg Pro Asp Gln Ala Arg
325 330 335

Met Asp Ile Arg Leu Ala Lys Thr Leu Val Leu Ile Leu Val Val Leu
340 345 350

Ile Ile Cys Trp Gly Pro Leu Leu Ala Ile Met Val Tyr Asp Val Phe
355 360 365

Gly Lys Met Asn Lys Leu Ile Lys Thr Val Phe Ala Phe Cys Ser Met
370 375 380

Leu Cys Leu Leu Asn Ser Thr Val Asn Pro Ile Ile Tyr Ala Leu Arg
385 390 395 400

Ser Lys Asp Leu Arg His Ala Phe Arg Ser Met Phe Pro Ser Cys Glu
405 410 415

Gly Thr Ala Gln Pro Leu Asp Asn Ser Met Gly Asp Ser Asp Cys Leu
420 425 430

His Lys His Ala Asn Asn Ala Ala Ser Val His Arg Ala Ala Glu Ser
435 440 445

Cys Ile Lys Ser Thr Val Lys Ile Ala Lys Val Thr Met Ser Val Ser
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Thr Asp Thr Ser Ala Glu Ala Leu
465 470

<210> 2

<211> 411

<212> PRT

<213> Human

<400> 2

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Thr Trp Ala Gln Met Thr Phe Ser Thr Lys Thr Ser Lys Glu Asn Glu
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Glu Asn Ile Gln Cys Gly Glu Asn Phe Met Asp Ile Glu Cys Phe Met
35 40 45

Val Leu Asn Pro Ser Gln Gln Leu Ala Ile Ala Val Leu Ser Leu Thr
50 55 60

Leu Gly Thr Phe Thr Val Leu Glu Asn Leu Leu Val Leu Cys Val Ile
65 70 75 80

Leu His Ser Arg Ser Leu Arg Cys Arg Pro Ser Tyr His Phe Ile Gly
85 90 95

Ser Leu Ala Val Ala Asp Leu Leu Gly Ser Val Ile Phe Val Tyr Ser
100 105 110

Phe Ile Asp Phe His Val Phe His Arg Lys Asp Ser Arg Asn Val Phe
115 120 125

Leu Phe Lys Leu Gly Gly Val Thr Ala Ser Phe Thr Ala Ser Val Gly
130 135 140

Ser Leu Phe Leu Thr Ala Ile Asp Arg Tyr Ile Ser Ile His Arg Pro
145 150 155 160

Leu Ala Tyr Lys Arg Ile Val Thr Arg Pro Lys Ala Val Val Ala Phe
165 170 175

Cys Leu Met Trp Thr Ile Ala Ile Val Ile Ala Val Leu Pro Leu Leu
180 185 190

Gly Trp Asn Cys Glu Lys Leu Gln Ser Val Cys Ser Asp Ile Phe Pro
195 200 205

His Ile Asp Glu Thr Tyr Leu Met Phe Trp Ile Gly Val Thr Ser Val
210 215 220

Leu Leu Leu Phe Ile Val Tyr Ala Tyr Met Tyr Ile Leu Trp Lys Ala
225 230 235 240

His Ser His Ala Val Arg Met Ile Gln Arg Gly Thr Gln Lys Ser Ile
245 250 255

Ile Ile His Thr Ser Glu Asp Gly Lys Val Gln Val Thr Arg Pro Asp
260 265 270

Gln Ala Arg Met Asp Ile Arg Leu Ala Lys Thr Leu Val Leu Ile Leu
275 280 285

Val Val Leu Ile Ile Cys Trp Gly Pro Leu Leu Ala Ile Met Val Tyr
290 295 300

Asp Val Phe Gly Lys Met Asn Lys Leu Ile Lys Thr Val Phe Ala Phe
305 310 315 320

Cys Ser Met Leu Cys Leu Leu Asn Ser Thr Val Asn Pro Ile Ile Tyr
325 330 335

Ala Leu Arg Ser Lys Asp Leu Arg His Ala Phe Arg Ser Met Phe Pro
340 345 350

Ser Cys Glu Gly Thr Ala Gln Pro Leu Asp Asn Ser Met Gly Asp Ser
355 360 365

Asp Cys Leu His Lys His Ala Asn Asn Ala Ala Ser Val His Arg Ala
370 375 380

Ala Glu Ser Cys Ile Lys Ser Thr Val Lys Ile Ala Lys Val Thr Met
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Ser Val Ser Thr Asp Thr Ser Ala Glu Ala Leu
405 410

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<212> PRT

<213> Human

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<210> 4

<211> 23

<212> PRT

<213> Human

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Ser Phe Arg Gly Ser Pro Phe
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<210> 5

<211> 20

<212> PRT

<213> Human

<400> 5

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Asn Ile Gln Cys
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<210> 6

<211> 20

<212> PRT

<213> Human

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Glu Asp Gly Lys
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<210> 7

<211> 12

<212> PRT

<213> Human

<400> 7

Val Tyr Asp Val Phe Gly Lys Met Asn Lys Leu Ile
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<210> 8

<211> 20

<212> PRT

<213> Human

<400> 8

His Lys His Ala Asn Asn Ala Ala Ser Val His Arg Ala Ala Glu Ser
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Cys Ile Lys Ser
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<210> 9

<211> 20

<212> PRT

<213> Human

<400> 9

His	Lys	His	Ala	Asn	Asn	Thr	Ala	Ser	Met	His	Arg	Ala	Ala	Glu	Ser
1				5					10					15	

Cys	Ile	Lys	Ser
			20